

FID/S (Ratio)														Type(s)		
Reduced Functions	Name	Symbol	Accession	1	p-val (1)	2	p-val (2)	3	p-val (3)	4	p-val (4)	5	p-val (5)	6	p-val (6)	Location
Mitochondrial Function	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	ATP5B	G3V6D3	0.86	0.00	0.95	0.15	0.84	0.00	1.28	0.00	0.85	0.00	0.91	0.01	Cytoplasm
	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	ATP5C1	Q6PCU0	0.88	0.01	0.95	0.21	0.86	0.01	1.27	0.00	0.92	0.23	0.97	0.54	Cytoplasm
	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1	ATP5F1	P19511	0.86	0.02	0.92	0.15	0.81	0.01	1.29	0.00	0.89	0.05	1.04	0.41	Cytoplasm
	cytochrome c oxidase subunit IV isoform 1	COX4I1	P19508	0.93	0.03	0.98	0.04	0.95	0.01	1.23	0.02	0.84	0.02	0.93	0.16	Cytoplasm
	cytochrome c oxidase subunit V	COX6C	P19591	0.93	0.24	1.01	0.88	0.82	0.03	1.20	0.04	0.84	0.02	0.94	0.55	Cytoplasm
	cytochrome c oxidase subunit VIIa polypeptide 2 like	COX7A2L	B2RYT5	0.88	0.08	0.94	0.36	0.82	0.03	1.20	0.04	0.89	0.11	0.98	0.80	Cytoplasm
	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	GPD2	P35571	0.94	0.03	0.95	0.19	0.91	0.00	1.24	0.00	1.01	0.70	0.95	0.09	Cytoplasm
	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	NDUF42	D3ZS58	0.89	0.05	0.74	0.11	0.85	0.03	1.22	0.03	0.87	0.18	0.93	0.26	Cytoplasm
	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	NDUF45	D63362	0.89	0.16	0.92	0.28	0.81	0.03	1.22	0.03	0.78	0.10	0.95	0.40	Cytoplasm
	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	NDUF49	O5BK63	0.91	0.01	0.94	0.07	0.80	0.00	1.25	0.00	1.07	0.06	0.97	0.49	Cytoplasm
	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	NDUFB10	D4AO7O	0.92	0.10	0.95	0.29	0.87	0.02	1.24	0.01	0.83	0.05	0.94	0.24	Cytoplasm
	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	NDUFH1	O66HF1	0.89	0.00	0.96	0.21	0.87	0.00	1.23	0.00	0.89	0.00	0.95	0.06	Cytoplasm
	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	NDUFH2	O641Y2	0.88	0.00	0.93	0.07	0.87	0.00	1.27	0.00	0.95	0.33	1.03	0.44	Cytoplasm
	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	NDUFH3	D3ZG43	0.92	0.11	0.96	0.44	0.84	0.00	1.23	0.00	0.87	0.04	0.92	0.30	Cytoplasm
	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	NDUFH4	O5XF13	0.89	0.06	0.94	0.26	0.78	0.00	1.30	0.01	0.88	0.22	0.97	0.86	Cytoplasm
	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	NDUFH8	B0BN6E	0.89	0.07	0.97	0.61	0.83	0.01	1.22	0.02	0.91	0.30	0.93	0.21	Cytoplasm
	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	NDUFV1	O5KH3	0.90	0.01	0.96	0.24	0.85	0.00	1.17	0.00	0.95	0.38	0.93	0.25	Cytoplasm
	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NDUFV2	P19234	0.86	0.04	0.96	0.51	0.85	0.02	1.26	0.00	0.95	0.57	0.99	0.92	Cytoplasm
	parkinson protein 7	PARK7	O88767	1.07	0.34	1.18	0.07	1.76	0.01	0.84	0.04	1.88	0.00	0.82	0.03	Nucleus
	pyruvate dehydrogenase (lipoyamide) alpha 1	PDHA1	O4FZ44	0.80	0.00	0.84	0.05	1.27	0.00	1.59	0.00	1.45	0.00	1.09	0.10	Cytoplasm
	peroxiredoxin 5	PRDX5	D3ZEN5	0.97	0.64	1.00	0.94	1.67	0.00	1.11	0.08	1.79	0.00	0.97	0.63	Cytoplasm
	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	SDHA	O920L2	0.95	0.12	0.94	0.29	0.88	0.00	1.21	0.00	0.91	0.15	1.01	0.86	Cytoplasm
	synuclein, alpha (non A4 component of amyloid precursor)	SNCA	P37377-2	1.18	0.06	1.15	0.07	2.03	0.00	1.02	0.75	1.50	0.02	1.00	0.98	Cytoplasm
	superoxide dismutase 2, mitochondrial	SOD2	P07895	0.98	0.77	1.03	0.68	1.76	0.00	1.11	0.13	1.22	0.03	0.94	0.29	Cytoplasm
	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UCRCR2	P32551	0.97	0.51	1.01	0.75	0.84	0.00	1.20	0.00	0.86	0.00	0.95	0.19	Cytoplasm
	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UCRCRFS1	P20788	0.91	0.10	0.99	0.85	0.86	0.02	1.21	0.00	0.87	0.01	0.99	0.82	Cytoplasm
Glutamate Receptor Signaling	glutaminase	GLS	P13264	0.90	0.01	0.94	0.08	1.46	0.00	1.36	0.00	1.70	0.00	1.04	0.26	Cytoplasm
	guanine nucleotide binding protein (G protein), beta polypeptide 1	GNB1	P54311	1.00	0.95	1.00	1.00	0.84	0.04	0.88	0.09	0.80	0.19	1.01	0.89	Plasma Membrane
	glutamate receptor, ionotropic, AMPA 3	GRIA3	P19492-2	0.94	0.13	0.87	0.01	0.67	0.00	1.21	0.00	0.80	0.00	1.01	0.64	Plasma Membrane
	glutamate receptor, ionotropic, N-methyl D-aspartate 1	GRIK1	O62683	1.00	0.92	0.95	0.10	0.80	0.00	0.89	0.00	0.77	0.00	1.01	0.20	Plasma Membrane
	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	GRIK2A	G3V9C5	1.00	0.96	0.94	0.15	0.80	0.00	0.88	0.03	0.79	0.00	1.02	0.51	Plasma Membrane
	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	GRIK2B	G3V746	1.01	0.69	0.95	0.14	0.82	0.00	0.93	0.05	0.82	0.01	1.04	0.30	Plasma Membrane
	glutamate receptor, metabotropic 3	GRM3	P31422	0.88	0.00	0.90	0.01	0.75	0.00	0.89	0.04	0.71	0.00	1.03	0.50	Plasma Membrane
	glutamate receptor, metabotropic 5	GRM5	B2CZ8C	1.02	0.77	0.96	0.46	0.79	0.01	0.92	0.22	0.86	0.36	1.08	0.15	Plasma Membrane
	glutamate receptor, metabotropic 7	GRM7	P35400	0.94	0.43	0.95	0.47	0.75	0.02	0.88	0.05	0.78	0.01	0.98	0.75	Plasma Membrane
	solute carrier family 1 (glial high affinity glutamate transporter), member 3	SLC1A1	G3V846	0.93	0.26	0.97	0.66	0.66	0.00	0.94	0.36	0.62	0.03	1.01	0.97	Plasma Membrane
	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	SLC1A4	P76GL9	0.81	0.01	0.81	0.01	0.61	0.00	0.90	0.60	0.85	0.22	0.91	0.33	Plasma Membrane
CREB Signaling	calcium/calmodulin-dependent protein kinase II alpha	CAMK2A	P11275	1.67	0.00	1.26	0.00	1.11	0.25	0.81	0.00	0.83	0.00	1.55	0.00	Cytoplasm
	calcium/calmodulin-dependent protein kinase II, beta	CAMK2B	G3V9G3	1.69	0.00	1.24	0.00	1.09	0.23	0.85	0.01	0.77	0.01	1.43	0.01	Cytoplasm
	calcium/calmodulin-dependent protein kinase II gamma	CAMK2G	P11730	1.57	0.00	1.33	0.00	1.12	0.12	0.89	0.17	0.89	0.17	1.33	0.13	Cytoplasm
	glutamate receptor, ionotropic, AMPA 3	GRIA3	P19492-2	0.94	0.13	0.87	0.01	0.67	0.00	1.21	0.00	0.80	0.00	1.01	0.05	Plasma Membrane
	glutamate receptor, metabotropic 2	GRM2	P31421	0.87	0.00	0.94	0.04	0.84	0.05	0.77	0.02	0.87	0.07	1.27	0.05	Plasma Membrane
	glutamate receptor, metabotropic 3	GRM3	P31422	0.88	0.00	0.90	0.01	0.75	0.00	0.89	0.04	0.71	0.00	1.03	0.50	Plasma Membrane
	inositol 1,4,5-trisphosphate receptor, type 1	ITPR1	P29994-8	0.99	0.70	0.90	0.01	0.84	0.00	1.04	0.37	0.83	0.01	1.06	0.22	Cytoplasm
	mitogen-activated protein kinase kinase 1	MAP2K1	Q01986	1.11	0.04	1.18	0.01	1.43	0.00	1.09	0.12	1.34	0.01	1.61	0.00	Cytoplasm
Increased Functions	glycolysis I	ALDOC	P09117	1.15	0.01	1.26	0.00	1.92	0.00	0.91	0.08	1.55	0.00	0.97	0.47	Cytoplasm
	aldolase C, fructose-biphosphate	ENO2	P07323	1.10	0.04	1.18	0.00	2.06	0.00	0.82	0.01	1.78	0.00	0.88	0.05	Cytoplasm
	enolase 2 (gamma, neuronal)	GAPDH	P04797	1.23	0.00	1.28	0.00	2.31	0.00	1.18	0.00	1.19	0.03	2.26	0.00	Cytoplasm
	glyceraldehyde-3-phosphate dehydrogenase	GPI	O6P6V0	1.15	0.00	1.20	0.00	2.07	0.00	0.81	0.00	2.22	0.00	0.85	0.01	Extracellular Space
	glucose-6-phosphate isomerase	PFKM	O52KS1	1.21	0.00	1.22	0.00	1.85	0.00	0.87	0.02	1.22	0.00	0.95	0.23	Cytoplasm
	malate dehydrogenase 1, NAD (soluble)	MDH1	O88989	1.13	0.01	1.14	0.01	1.99	0.00	0.85	0.02	1.81	0.01	0.93	0.37	Cytoplasm
	malate dehydrogenase 2, NAD (mitochondrial)	MDH2	P04636	0.93	0.06	1.06	0.12	2.12	0.00	1.23	0.01	1.40	0.00	0.99	0.76	Cytoplasm
	malic enzyme 3, NADP(+)-dependent, mitochondrial	ME3	F1M5N4	0.84	0.01	0.89	0.07	1.58	0.00	1.43	0.00	1.56	0.02	1.18	0.02	Cytoplasm
	phosphoglycerate kinase 1	PGK1	P16617	1.03	0.11	1.37	0.03	1.80	0.00	0.74	0.00	1.73	0.00	0.77	0.00	Cytoplasm
Gluconeogenesis I	enolase 2 (gamma, neuronal)	ENO2	P07323	1.10	0.04	1.18	0.00	2.06	0.00	0.82	0.01	1.78	0.00	0.88	0.05	Cytoplasm
	glyceraldehyde-3-phosphate dehydrogenase	GAPDH	P04797	1.23	0.00	1.28	0.00	2.31	0.00	1.18	0.00	1.19	0.03	2.26	0.00	Cytoplasm
	glucose-6-phosphate isomerase	GPI	O6P6V0	1.15	0.00	1.20	0.00	2.07	0.00	0.81	0.00	2.22	0.00	0.85	0.01	Extracellular Space
	malate dehydrogenase 1, NAD (soluble)	MDH1	O88989	1.13	0.01	1.14	0.01	1.99	0.00	0.85	0.02	1.81	0.01	0.93	0.37	Cytoplasm
	malate dehydrogenase 2, NAD (mitochondrial)	MDH2	P04636	0.93	0.06	1.06	0.12	2.12	0.00	1.23	0.01	1.40	0.00	0.99	0.76	Cytoplasm
	malic enzyme 3, NADP(+)-dependent, mitochondrial	ME3	F1M5N4	0.84	0.01	0.89	0.07	1.58	0.00	1.43	0.00	1.56	0.02	1.18	0.02	Cytoplasm
14-3-3 Mediated Signaling	mitogen-activated protein kinase kinase 1	MAP2K1	Q01986	1.11	0.04	1.18	0.01	1.43	0.00	0.91	0.12	1.34	0.01	0.94	0.26	Cytoplasm
	tubulin, beta class III	TUBB3	Q4QR84	1.15	0.11	1.26	0.03	1.91	0.00	0.84	0.27	1.50	0.03	0.85	0.46	Cytoplasm
	tubulin, beta class I	TUBB	P69897	1.24	0.06	1.34	0.03	1.73	0.01	0.84	0.19	1.24	0.14	0.77	0.21	Cytoplasm
	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	YWHAE	P62260	1.05	0.28	1.10	0.04	1.74	0.00	0.96	0.33	1.76	0.01	0.94	0.25	Cytoplasm
	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	YWHAQ	P68255	1.11	0.17	1.18	0.05	1.85	0.00	0.95	0.03	1.84	0.01	0.87	0.14	Cytoplasm
	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	YWHAZ	P61983	1.03	0.24	1.15	0.02	2.12	0.10	0.92</td						